

```

<!--StartFragment-->RESULT 7
Y1610_METJA
ID Y1610_METJA Reviewed; 615 AA.
AC Q59005;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 26-FEB-2008, entry version 47.
DE Uncharacterized glycosyl hydrolase MJ1610 (EC 3.2.1.-).
GN OrderedLocusNames=MJ1610;
OS Methanocaldococcus jannaschii (Methanococcus jannaschii).
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 15 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; L77117; AAB99630.1; -; Genomic_DNA.
DR PIR; A64501; A64501.
DR RefSeq; NP_248620.1; -.
DR GeneID; 1452519; -.
DR GenomeReviews; L77117_GR; MJ1610.
DR KEGG; mja:MJ1610; -.
DR TIGR; MJ1610; -.
DR BioCyc; MJAN243232:MJ_1610-MON; -.
DR InterPro; IPR012341; 6hp_glycosidase.
DR InterPro; IPR006465; Glucoamylase.
DR InterPro; IPR000165; Glyco_hydro_15.
DR InterPro; IPR011613; Glyco_hydro_15_rel.
DR Gene3D; G3DSA:1.50.10.10; CelA/Cel48F_cat; 1.
DR Pfam; PF00723; Glyco_hydro_15; 1.
DR TIGRFAMs; TIGR01577; oligosac_amy1; 1.
DR PROSITE; PS00820; GLUCOAMYLASE; 1.
PE 3: Inferred from homology;
KW Complete proteome; Glycosidase; Hydrolase.
FT CHAIN 1 615 Uncharacterized glycosyl hydrolase
FT MJ1610.
FT /FTId=PRO_0000186121.
FT ACT_SITE 403 403 Proton acceptor (By similarity).
FT ACT_SITE 406 406 Proton donor (By similarity).
SQ SEQUENCE 615 AA; 72008 MW; 2B37EB89F0357BE5 CRC64;

Query Match 55.0%; Score 1841.5; DB 1; Length 615;
Best Local Similarity 51.5%; Pred. No. 3e-113;
Matches 320; Conservative 143; Mismatches 149; Indels 9; Gaps 5;

```

```

Qy      1  MAGIIGNGNLLAKIDDLGSIEYIFFPHLGYETHILDTSAFYNNKIKWHWDHSDVDSQN  60
      | :|:| :|:| | | :|:|:| :|:| | :| :| :| :|:| | :|:|
Db      4  MGGIVGNNSLLAKIGDYGEIYLFYPQVGYETHFFDSALAV-YDKKVKWHWDHDDWIDITQK  62

Qy     61  YLKDSNLIKTTYENDFLIYSKDCVSISHNLIVKQLSIINKTNSKEDIKFFYENLRIGE  120
      |:|:| | | :| :| :| | :|:|:|:| :| :| :| :| :|:|:|:|
Db     63  YIEETHIFKTILEDDEKIIILTIDKFVPVSHNVLIIRVYIKNKLDKKLNFKLFFYENLRIGE  122

Qy    121  TPSKSTVFKVKEKNCLIKHDKNYIFCIGSNKKVSSYQCIGIKYSESSALRDIENGVLKEQS  180
      | :|:| | | :|:| :|:|:|:|:| :|:|:|:|:| :|:|:|:|
Db    123  NPITNTVKFL-EDGCIVKNGKYIFCIGSDKRIDSFCQGNRYSKTSAYDIENTIGLKEHK  181

Qy    181  SATGLITDSALCWEFKIKPNQRYTSLILPEKYDGDYKNTLNLMDTLHMVKDNLKDLYN  240
      :|:|:|:| | | :| :| :|:|:|:|:| :| :| :| :| :|:|
Db    182  ESSGLLTDSAISWNKIDEKRSALFNIYILPQRFDGDFS--IITEQLKIIMNSENIN  238

Qy    241  LTRNFWSRVDMSVKNWGILKEEYKECIDICKRSLTLTLLLCDYKGGIIASPSLHPDYR  300
      | :|:| :| :|:| :| :| :| :| :|:|:|:| :|:|:|:|:|
Db    239  LSMNYWK-HIIGEINRFIHPQLRQNNKIYSITKRALMTLLMLCDKEGGIIAAPS LHPDYR  297

Qy    301  YVWCRDAGYMAVALDLCGQHEMSEKYFEWCKTTQNSDGSWVQNYVVEGYPRFTAIQIDQV  360
      | | | | :|:|:| | :| :|:|:| :|:|:|:|:| | | | | | |
Db    298  YVWGRDGSYISIALDLFGIRNIPDRFFEFSKIQNADGSWLQNYVNGKPRLTAIQTDQI  357

Qy    361  GTTIWALLVHYRITGDKHFLKRNWEMVKKAGDYLSRAADQLIPCYDLWEEKFGVFAYTLG  420
      | :|:| :|:|:|:| :|:| | :|:| | | :|:|:|:|:|:|:|
Db    358  GSILWAMDVHYRLTGDRKFVERYWNTIEKAANYLRLVALNFTPCFDLWEERFGVFAYTMG  417

Qy    421  AIYGGKLSGYLICKELDKKEEIQHWKKS MNFLKNEVVNRLYLKNEKRFKSLKPLDKTID  480
      | | | | | :| :| :|:| :| :|:|:| | :|:|:|:|:| :|:|:|
Db    418  ATYAGLKCAYSMSKAVNKRDKVKDWGKTIEFLKHEVPKRFYLEDEERFAKSINPLDKTID  477

Qy    481  TSILGLSFPYGLVSVDDPRIISTANQIEKAFNYKVGGVGRYPEDIYFGGNPWIIITLWLY  540
      | | | |:| :| :| :| | | | | | | | | | | | | | | | |
Db    478  TSILGLSYFPNLIDVDDERMIKTAEAIEKAFKYKVGIGGRYPEDIYFGGNPWIIITLWLS  537

Qy    541  MYKKLVDTLSKKGKFQESIIDNYNKKCNLLKWILKHQFNGMFPEQVHKDLGIPISAIP  600
      |:|:| | :| :| :| :| | | :|:| :|:|:|:|:|:|:|:|:|
Db    538  LYYRRLYKVLKEK---DDNGADIYLKSKKLFNVVMKYSFDGLFPEQIHKELGVPM SAMP  594

Qy    601  LGWSHAMVIIAHGDYDILIP  621
      | | | :| :| :| :| :|
Db    595  LGWSNAMFLIYVYENDKVIIP  615
<!--EndFragment-->

```